

## SEQUENCE LISTING

<110> Viaxxel Biotech GmbH

<120> Compounds that affect CD83 expression, pharmaceutical compositions comprising said compounds and methods for identifying said compounds

<130> 84201

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<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(615)

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10025367 121901

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 65 70 75 80

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 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn  
 85 90 95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg 336  
 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro  
 100 105 110

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 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly  
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 145 150 155 160

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<213> Homo sapiens

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Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser

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Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln

50

55

60

Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly

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75

80

Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn

85

90

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Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro

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105

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Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly

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Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu

10025367 "121901"

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135

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Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile

145

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155

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Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser

165

170

175

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys

180

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His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val

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&lt;210&gt; 3

&lt;211&gt; 2051

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (14)..(601)

&lt;400&gt; 3

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gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct 97

Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala

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tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag 145

Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln

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 Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro  
 65 70 75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc 289  
 Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser  
 80 85 90

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 Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn  
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 Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe  
 125 130 135 140

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 Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe  
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gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa 529  
 Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu  
 160 165 170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg 577  
 Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val  
 175 180 185

10025367 121301

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 190 195  
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tcagccatga ctttcatgct attaaaagaa tgcattgtgaa 2051

<213> Mus musculus

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Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr  
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Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr  
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Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val  
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Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln  
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Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu  
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cag gat gag tta cga agc ctg ttc agc agc att ggt gaa gtt gaa tct 144  
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gca aaa ctt att cgg gat aaa gta gca gga cac agc ttg ggc tac ggc 192  
 Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly  
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 Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr  
 65 70 75 80

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 85 90 95

cgc ccg agc tca gag gtg atc aaa gac gcc aac ttg tac atc agc ggg 336  
 Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly  
 100 105 110

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 115 120 125

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 Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly  
 130 135 140

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 Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser  
 165 170 175  
  
 gag ccc atc gca gtg aag ttt gca gcc aac ccc aac cag aac aaa aac 576  
 Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn  
 180 185 190  
  
 gtg gca ctc ctc tcg cag ctg tac cac tcg cca gcg cga cgg ttc gga 624  
 Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly  
 195 200 205  
  
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 Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly  
 210 215 220  
  
 gtc gat cac atg agc ggg ctc tct ggc gtc aac gtg cca gga aac gcc 720  
 Val Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala  
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 245 250 255  
  
 gag ggg atc ctc tgg cag atg ttt ggg ccg ttt ggt gcc gtc acc aat 816  
 Glu Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn  
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 Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly  
 275 280 285  
  
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 Phe Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser

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ctg aac ggc tac cgc ctg ggg gac aaa atc tta cag gtt tcc ttc aaa 960

Leu Asn Gly Tyr Arg Leu Gly Asp Lys Ile Leu Gln Val Ser Phe Lys

305

310

315

320

acc aac aag tcc cac aaa taa

981

Thr Asn Lys Ser His Lys

325

&lt;210&gt; 6

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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20

25

30

Gln Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser

35

40

45

Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly

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55

60

Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr

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70

75

80

Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala

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90

95

Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly

100

105

110

10025367 121901

Leu Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg  
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Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly  
 130 135 140

Leu Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala  
 145 150 155 160

Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser  
 165 170 175

Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn  
 180 185 190

Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly  
 195 200 205

Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly  
 210 215 220

Val Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala  
 225 230 235 240

Ser Ser Gly Trp Cys Ile Phe Ile Tyr Asn Leu Gly Gln Asp Ala Asp  
 245 250 255

Glu Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn  
 260 265 270

Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly  
 275 280 285

Phe Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser  
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10025367 121901

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Thr Asn Lys Ser His Lys

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

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&lt;211&gt; 1077

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

10025367 121901



&lt;220&gt;

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&lt;222&gt; (1)..(1077)

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Gly Pro Thr Thr Ile Asn Asn Asn Cys Ser Ser Pro Val Asp Ser Gly	
20 25 30	
aac aca gaa gac agc aag acc aac tta ata gtc aac tac ctt cct cag	144
Asn Thr Glu Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln	
35 40 45	
aac atg aca cag gag gaa cta aag agt ctc ttt ggg agc att ggt gaa	192
Asn Met Thr Gln Glu Glu Leu Lys Ser Leu Phe Gly Ser Ile Gly Glu	
50 55 60	
ata gag tcc tgt aag ctt gta aga gac aaa ata aca ggg cag agc ttg	240
Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Gln Ser Leu	
65 70 75 80	
gga tat ggc ttt gtg aac tac att gac ccc aag gat gca gag aaa gct	288
Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala	
85 90 95	
atc aac acc ctg aat gga ttg aga ctt caa acc aaa aca ata aaa gtt	336
Ile Asn Thr Leu Asn Gly Leu Arg Leu Gln Thr Lys Thr Ile Lys Val	
100 105 110	
tcc tat gct cgc cca agt tca gct tct atc aga gat gca aat tta tat	384
Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr	
115 120 125	

10025367 121901

gtc agc gga ctt cca aaa aca atg acc cag aag gag ttg gaa cag ctt 432  
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 Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln  
 145 150 155 160

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 Val Thr Gly Ile Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg  
 165 170 175

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 Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Pro  
 180 185 190

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 Gly Ala Thr Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln  
 195 200 205

aaa acc aat cag gcc atc ctt tcc cag ctg tac cag tct cca aac aga 672  
 Lys Thr Asn Gln Ala Ile Leu Ser Gln Leu Tyr Gln Ser Pro Asn Arg  
 210 215 220

agg tat cca gga ccg cta gct cag cag gca cag cgt ttt agg ttg gac 720  
 Arg Tyr Pro Gly Pro Leu Ala Gln Gln Ala Gln Arg Phe Arg Leu Asp  
 225 230 235 240

aat ctg ctc aat atg gct tat gga gta aag agg ttt tct cca atg acc 768  
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 245 250 255

att gac gga atg acc agt ttg gct gga att aat atc cct ggg cac cct 816  
 Ile Asp Gly Met Thr Ser Leu Ala Gly Ile Asn Ile Pro Gly His Pro  
 260 265 270

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Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu Ala Pro Asp Ala Asp

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280

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gag agt atc ctg tgg caa atg ttt ggg cct ttt gga gct gtc acc aat 912

Glu Ser Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn

290

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300

gtg aag gtc atc cgt gac ttt aac acc aat aaa tgc aaa ggt ttt gga 960

Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly

305

310

315

320

ttt gtg act atg aca aac tat gat gag gct gcc atg gcg ata cgt agc 1008

Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Arg Ser

325

330

335

ctc aat gga tac cgt ctg gga gac aga gta ctg cag gtc tcc ttt aag 1056

Leu Asn Gly Tyr Arg Leu Gly Asp Arg Val Leu Gln Val Ser Phe Lys

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345

350

aca aac aaa acg cac aaa gcc

1077

Thr Asn Lys Thr His Lys Ala

355

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<400> 23

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Gly Pro Thr Thr Ile Asn Asn Asn Cys Ser Ser Pro Val Asp Ser Gly

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25

30

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Asn Thr Glu Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln  
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Asn Met Thr Gln Glu Glu Leu Lys Ser Leu Phe Gly Ser Ile Gly Glu  
 50 55 60

Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Gln Ser Leu  
 65 70 75 80

Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala  
 85 90 95

Ile Asn Thr Leu Asn Gly Leu Arg Leu Gln Thr Lys Thr Ile Lys Val  
 100 105 110

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr  
 115 120 125

Val Ser Gly Leu Pro Lys Thr Met Thr Gln Lys Glu Leu Glu Gln Leu  
 130 135 140

Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln  
 145 150 155 160

Val Thr Gly Ile Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg  
 165 170 175

Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Pro  
 180 185 190

Gly Ala Thr Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln  
 195 200 205

Lys Thr Asn Gln Ala Ile Leu Ser Gln Leu Tyr Gln Ser Pro Asn Arg  
 210 215 220

Arg Tyr Pro Gly Pro Leu Ala Gln Gln Ala Gln Arg Phe Arg Leu Asp

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225                      230                      235                      240  
 Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser Pro Met Thr  
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 Ile Asp Gly Met Thr Ser Leu Ala Gly Ile Asn Ile Pro Gly His Pro  
                     260                      265                      270  
 Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu Ala Pro Asp Ala Asp  
                     275                      280                      285  
 Glu Ser Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn  
                     290                      295                      300  
 Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly  
 305                      310                      315                      320  
 Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Arg Ser  
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Pro Ala Gly Pro Ala Leu Pro Asn Gly Pro Leu Leu Gly Thr Asn Gly

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30

gcc act gac gac agc aag acc aac ctc atc gtc aac tac ctg ccc cag 144

Ala Thr Asp Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln

35

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45

aac atg acc cag gat gag ttc aag agt ctc ttc ggc agc att ggc gac 192

Asn Met Thr Gln Asp Glu Phe Lys Ser Leu Phe Gly Ser Ile Gly Asp

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Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Arg Asp Leu

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ggc tac ggg ttt gtg aac tat cct gac ccc aat gat gca gac aaa gcc 288

Gly Tyr Gly Phe Val Asn Tyr Pro Asp Pro Asn Asp Ala Asp Lys Ala

85

90

95

atc aac acc ctc aac ggc ctc aaa tta cag acg aag acc atc aag gtg 336

Ile Asn Thr Leu Asn Gly Leu Lys Leu Gln Thr Lys Thr Ile Lys Val

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105

110

tcc tat gcc aga ccc agt tca gca tcc atc cgg gat gct aac ctg tac 384

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr

115

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gtc agc ggg ctc ccc aag acc atg agc cag aaa gag atg gag cag ctc 432

Val Ser Gly Leu Pro Lys Thr Met Ser Gln Lys Glu Met Glu Gln Leu

130

135

140

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gtc aca ggt gtc tct cgg ggt gtg gga ttc atc cgc ttt gac aag agg 528  
 Val Thr Gly Val Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg  
 165 170 175

att gag gcc gaa gag gct atc aaa gga ctg aat ggg cag aag ccg ctg 576  
 Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Leu  
 180 185 190

ggc gca gct gag ccc atc aca gtc aag ttc gcg aac aac cca agt cag 624  
 Gly Ala Ala Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln  
 195 200 205

aag acg ggg cag gcg ctg ctc acc cac ctc tac cag tca tcc gcc cgg 672  
 Lys Thr Gly Gln Ala Leu Leu Thr His Leu Tyr Gln Ser Ser Ala Arg  
 210 215 220

cgc tac gca ggc ccc cta cac cat cag acc cag cgt ttc cgg ctg gac 720  
 Arg Tyr Ala Gly Pro Leu His His Gln Thr Gln Arg Phe Arg Leu Asp  
 225 230 235 240

aat ttg ctc aac atg gcc tac ggc gtc aag agg ttc tcg ccg atc gcc 768  
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 245 250 255

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 Ile Asp Gly Met Ser Gly Leu Ala Gly Val Gly Leu Ser Gly Gly Ala  
 260 265 270

gcg ggc ggc tgg tgc atc ttc gtg tac aac ctg tca ccg gag gca gac 864  
 Ala Gly Gly Trp Cys Ile Phe Val Tyr Asn Leu Ser Pro Glu Ala Asp  
 275 280 285

gag agc gtg ctg tgg cag ctg ttc ggg cct ttt ggg gca gtc acc aac 912

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Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe Gly Ala Val Thr Asn  
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 Val Lys Val Ile Arg Asp Phe Thr Thr Asn Lys Cys Lys Gly Phe Gly  
 305 310 315 320

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 Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Ala Ser  
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ctg aac ggc tat cgc ctg gcc gag cgc gtg ctg cag gtc tcc ttc aag 1056  
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 35 40 45

Asn Met Thr Gln Asp Glu Phe Lys Ser Leu Phe Gly Ser Ile Gly Asp  
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Gly Tyr Gly Phe Val Asn Tyr Pro Asp Pro Asn Asp Ala Asp Lys Ala  
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Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr  
115 120 125

Val Ser Gly Leu Pro Lys Thr Met Ser Gln Lys Glu Met Glu Gln Leu  
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Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln  
145 150 155 160

Val Thr Gly Val Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg  
165 170 175

Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Leu  
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Gly Ala Ala Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln  
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Lys Thr Gly Gln Ala Leu Leu Thr His Leu Tyr Gln Ser Ser Ala Arg  
210 215 220

Arg Tyr Ala Gly Pro Leu His His Gln Thr Gln Arg Phe Arg Leu Asp  
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 Thr Ser Asn Thr Ser Asn Gly Pro Ser Ser Asn Asn Arg Asn Cys Pro  
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tct ccc atg caa aca ggg gca acc aca gat gac agc aaa acc aac ctc 144  
 Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu  
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 Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser  
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ctc ttc ggg agc att ggt gaa ata gaa tcc tgc aaa ctt gtg aga gac 240  
 Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp  
 65 70 75 80

aaa att aca gga cag agt tta ggg tat gga ttt gtt aac tat att gat 288  
 Lys Ile Thr Gly Gln Ser Leu Gly Tyr Gly Phe Val Asn Tyr Ile Asp  
 85 90 95

cca aag gat gca gag aaa gcc atc aac act tta aat gga ctc aga ctc 336  
 Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu  
 100 105 110

cag acc aaa acc ata aag gtc tca tat gcc cgt ccg agc tct gcc tca 384  
 Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser  
 115 120 125

atc agg gat gct aac ctc tat gtt agc ggc ctt ccc aaa acc atg acc 432  
 Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr  
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cag aag gaa ctg gag caa ctt ttc tcg caa tac ggc cgt atc atc acc 480  
 Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr  
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ctg aat ggc cag aag ccc agc ggt gct acg gaa ccg att act gtg aag 624  
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 195 200 205

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 210 215 220

ctc tac cag tcc cct aac cgg cgc tac cca ggt cca ctt cac cac cag 720  
 Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln  
 225 230 235 240

gct cag agg ttc agg ctg gac aat ttg ctt aat atg gcc tat ggc gta 768  
 Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val  
 245 250 255

aag aga ctg atg tct gga cca gtc ccc cct tct gct tgt tcc ccc agg 816  
 Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg  
 260 265 270

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 Phe Ser Pro Ile Thr Ile Asp Gly Met Thr Ser Leu Val Gly Met Asn  
 275 280 285

atc cct ggt cac aca gga act ggg tgg tgc atc ttt gtc tac aac ctg 912  
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tcc ccc gat tcc gat gag agt gtc ctc tgg cag ctc ttt ggc ccc ttt 960  
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305                      310                      315                      320  
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                          325                      330                      335  
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 Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu  
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 Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser  
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Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp  
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85 90 95

Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu  
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Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser  
115 120 125

Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr  
130 135 140

Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr  
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Ser Arg Ile Leu Val Asp Gln Val Thr Gly Val Ser Arg Gly Val Gly  
165 170 175

Phe Ile Arg Phe Asp Lys Arg Ile Glu Ala Glu Glu Ala Ile Lys Gly  
180 185 190

Leu Asn Gly Gln Lys Pro Ser Gly Ala Thr Glu Pro Ile Thr Val Lys  
195 200 205

Phe Ala Asn Asn Pro Ser Gln Lys Ser Ser Gln Ala Leu Leu Ser Gln  
210 215 220

Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln  
225 230 235 240

Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val  
245 250 255

Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg

10025367 121901

270

Gln Val Ser Phe Lys Thr Asn Lys Ala His Lys Ser  
370 375 380